

Practitioner's Docket No. **MPI01-019P1RNM**

PATENT

In re application of:	Olandt, Peter J. et al.		
Application No.:	10/074,527	Group No.:	1652
Filed:	February 12, 2002	Examiner:	Rao, Manjunath N.
For:	33945, A HUMAN GLYCOSYLTRANSFERASE AND USES THEREFOR		

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

DECLARATION UNDER 37 C.F.R. § 1.131

Sir:

We, Peter J. Olandt, Rachel E. Meyers, and Katherine M. Galvin hereby declare and state:

1. In the United States, the conception of the sequence of the human 33945 molecules of the invention and the identification of the 33945 polypeptide as a glycosyltransferase occurred prior to December 15, 2000 and the reduction to practice comprising obtaining the final sequence known as SEQ ID NO:1 in the above-identified application was performed with due diligence until December 18, 2000, the date of the actual reduction to practice.
2. Evidence of conception prior to December 15, 2000 is provided in Exhibits A1-A3, which are copies of electronic printouts of a map of clones contributing to the 33945 nucleotide sequence and analyses of early 33945 sequences.

Exhibit A1 is a copy of page 1 of a Sequencher™ map identifying the clones contributing to the 33945 nucleotide sequence, the clone sizes and the positions of the clones relative to the 33945 sequence known at that stage of the invention process. Exhibit A2 is a copy of a BLAST analysis of a translation of that nucleotide sequence. The map was compiled and the analysis was

CERTIFICATION UNDER 37 C.F.R. SECTIONS 1.8(a) and 1.10*

I hereby certify that, on the date shown below, this correspondence is being:

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- ☒ deposited with the United States Postal Service in an envelope addressed to the Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.
37 C.F.R. SECTION 1.8(a)

37 C.F.R. SECTION 1.10*

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TRANSMISSION

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Signature

Sean Hunziker/Beverly Sotiropoulos

Date: August 9, 2004

(type or print name of person certifying)

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performed prior to December 15, 2000. By that time, the sequence was extensive, spanning 2109 nucleotides, and the BLAST revealed similarity of the 33945 polypeptide to glycosyltransferases. Exhibit A3 is a copy of a series of analyses performed on the polypeptide encoded by that 33945 nucleotide sequence. Page 1 of this printout bears the nearly complete polypeptide sequence known at the time, showing that it has the full length of 581 amino acids, but a few uncertain residues; page 3 bears the results of a Pfam analysis which matched a portion of the 33945 sequence with the Pfam Glycosyl transferase domain consensus sequence; pages 4 and 5 bear the results of an analysis which matched portions of the 33945 polypeptide sequence with glycosyltransferase domain consensus sequences from the ProDom database. The combined result of the analyses was the determination that the 33945 molecules of the invention represent a glycosyltransferase.

The original printouts in Exhibits A1-A3 bear the automatically embedded dates on which the analyses were performed. In accordance with accepted practice, the dates on the copies of the electronic printouts have been masked (M.P.E.P. § 715.07).

3. Evidence of the exercise of due diligence in the process of reducing to practice the 33945 molecules of the invention is provided in Exhibits B1-B5. In accordance with M.P.E.P. § 715.07, the actual dates of the acts portrayed in Exhibits B1-B5 have been provided to establish diligence. In accordance with M.P.E.P. § 715.07(a), the acts performed just prior to the effective date of December 15, 2000 until the December 18, 2000 date of the actual reduction to practice are included in Exhibits B1-B5.

Exhibit B1 is a copy of page 1 of an updated Sequencher™ map compiling the clones contributing to the 33945 nucleotide sequence as understood by November 27, 2000. One can see from this Exhibit, additional 5' clones "fbhX33945phg01b1.abi" and fbhX33945phh01b1.abi" which were not present on Exhibit A1. In addition, Exhibit B1 has a note written by inventor Peter Olandt, describing a 2 base pair problem needing to be solved. In order to solve this problem, additional clones were prepared to cover the region in question. This clone preparation process yielded four additional 5' clones, "fbhX33945peb04h1," "fbhX33945pee03g1," "fbhX33945pfd04h1" and "fbhX33945pfg03g1."

Clone fbhX33945pee03g1 is used herein as an example of the timecourse and types of analyses performed on these clones to show due diligence. Exhibit B2 provides a summary of the facts related to clone fbhX33945pee03g1, together with its nucleotide sequence. At the top of Exhibit B2, one can see that this clone was submitted for sequencing on December 12, 2000. As seen in the middle of the Exhibit, fbhX33945pee03g1 came out of sequencing on December 14, 2000 and was submitted for analyses. The first analysis was performed on December 14, 2000, and subsequent analyses were performed on December 15 and 16, 2000.

Exhibit B3 shows that on Monday, December 18, 2000, the four new clones were assembled into a new Sequencher™ clone map. The problem of base pair selection was solved and the complete 33945 nucleic acid sequence ("Fbh33945FL"), known in the application as SEQ ID NO:1 was finalized and submitted to the Millennium database on Monday, December 18, 2000, as shown on Exhibit B4. Exhibit B5, also performed on December 18, 2000, shows that analyses performed on the polypeptide encoded by the complete nucleotide sequence supported the earlier conclusion of 33945 as a glycosyltransferase drawn from the evidence of prior conception provided in Exhibits A2 and A3.

We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or

imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Peter J. Olandt

Date

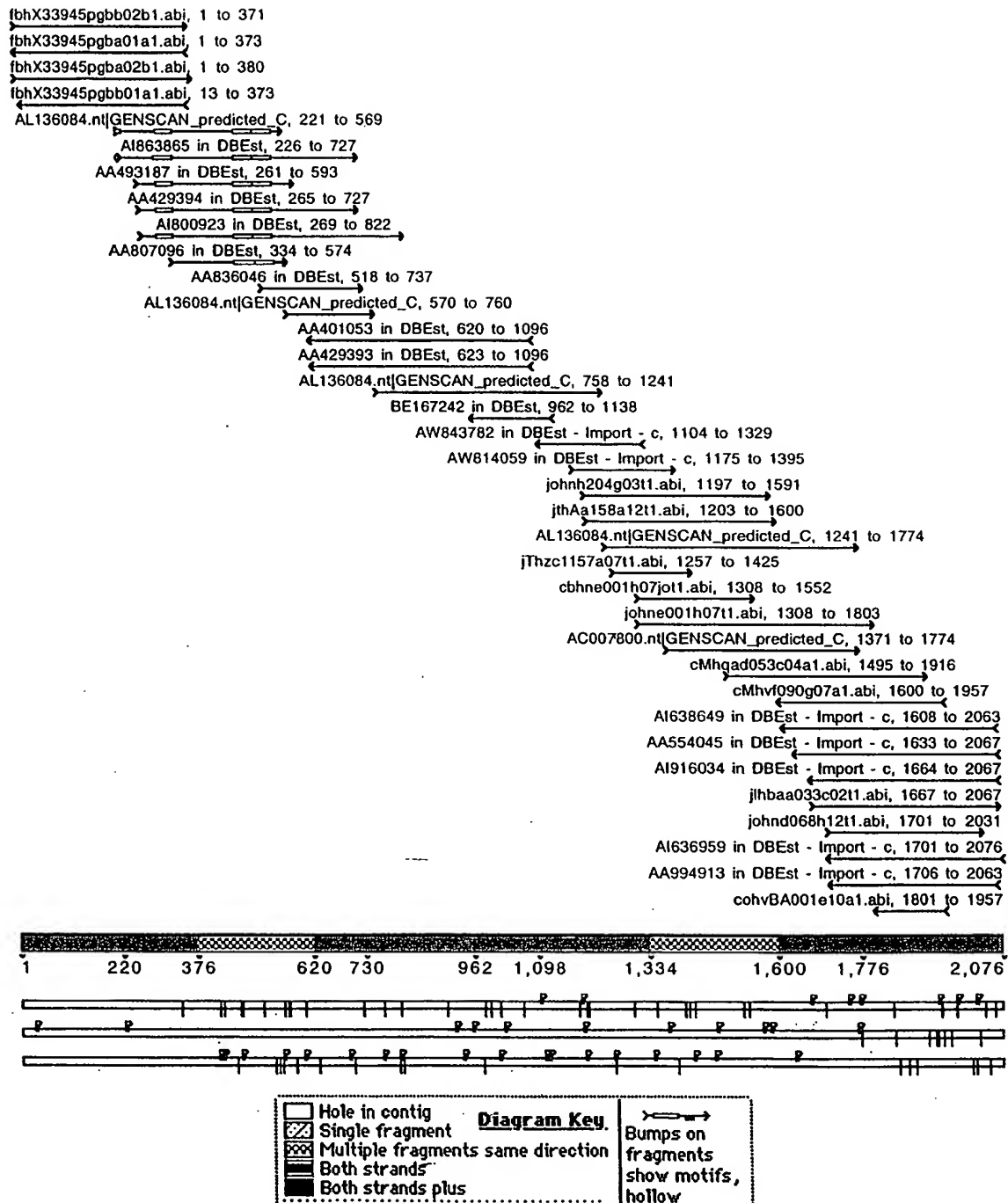
Rachel E. Meyers

Date

Katherine M. Galvin
Katherine M. Galvin

7-16-04
Date

33945
Sequencher™ "33945"



33945 (analysis only) (2109 bases) -
WU2 BLAST vs. PROT - Selected Database Hits

>gi|2121220|gb|AAB58301| (U73819) polypeptide GalNAc transferase-T4 [Mus
musculus]
Length = 578

Plus Strand HSPs:

Score = 1654 (587.3 bits), Expect = 3.7e-169, P = 3.7e-169
Identities = 328/570 (57%), Positives = 405/570 (71%), Frame = +2

Query: 128 VLLALLALAGL-----GSVLRAQRGAGAGAAEPGPRTPRPGRRE-----PVMRPPVPA 277
+LLALL LA + S L A GAG GA E GP R P RE P+ +PP +
Sbjct: 13 LLLALLTLAYILVEFSVSTLYASPGAG-GARELGPRRLPDLDTREEDLSQPLYIKPPADS 71

Query: 278 NALGARGEAVRLQLQGEELRLQESVRLHQINIYLSDRISLHRRLPXRWNPLCKEKKYDY 457
+ALG G A +LQL EL+ QEE + + INIYLSDRISLHR + + CK KK+ Y
Sbjct: 72 HALGEWGRASKLQLNEGELKQQEELIERYAINIYLSDRISLHRHIEDKRMYECKAKKFHY 131

Query: 458 DNLPRTSVIIAFYNEAWSTLLRTVYSVLETSFDILLEEVILVDDYSDREHLKERLANELS 637
+LP TSVIIAFYNEAWSTLLRT++SVLETSF +LL+E+ILVDD SDR +LK +L +S
Sbjct: 132 RSLPTTSVIIAFYNEAWSTLLRTIHSVLETSFAVLLKEIILVDDLSDRIYLKAQLEYIS 191

Query: 638 GLPKVRLIRANKREGLVRARLLGASAARGDVLTFDCHCECHGWLEPLLQRIHEEESAV 817
L +VRLIR NKREGLVRARL+GA+ A GDVLTFDCHCEC+ GWLEPLL+RI +E+A+
Sbjct: 192 NLERVRLIRTNKREGLVRARLIGATFATGDVLTFDCHCECNTGWLEPLLERISRDETAI 251

Query: 818 VCPVIDVIDWNTFEYLGNSGEPQIGGFDWRLVFTWHTVPERERIRMQSPVDVIRSPTMAG 997
VCPVID IDWNTFE+ +GEP IGGFDWRL F WH+VP+ ER R S +D IRSPTMAG
Sbjct: 252 VCPVIDTIDWNTFEFYMQTGPEMIGGFDWRLTFQWHSVPKHERDRRTSRIDPIRSPTMAG 311

Query: 998 GLFAVSKKYFEYLGSYDTGMEVWGGENLEFSFRIWQCGGVLETHPCSHVGHVFRKQAPYS 1177
GLFAVSKKYF+YLG+YDTGMEVWGGENLE SFR+WQCGG LE HPCSHVGHVF K+APY+
Sbjct: 312 GLFAVSKKYFQYLGTYDTGMEVWGGENLELSFRVWQCGGKLEIHPCSHVGHVFPKRAPYA 371

Query: 1178 RNKALANSVXAAEVWMDEFKELYHRNPRARLEPFGDVTERKQLRDKLQCKDFKWFLETV 1357
R L N+ AAEVWMDE+KE +Y+RNP AR E +GD++ERK LR++L+CK F W+L+ V
Sbjct: 372 RPNFLQNTARAAEVWMDEYKEHFYNRNPPARKEAYGDLSEKLLRERLCKCSFDWYLKNV 431

Query: 1358 YPELHVPEDRPGFFGMLQNKGLTDYCFDYNPPDENQIVGHQVILYLCHGMQGNQFFEYTS 1537
+ LHVPEDRPG+ G +++ G++ C DYN PD N G + L+ CHG G NQFFEYTS
Sbjct: 432 FSNLHVPEDRPGWHGAIRSMGISSECLDYNAPDNNP-TGANLSLFGCHGQGGNQFFEYTS 490

Query: 1538 QKEIRYNTHQPEGCIAVEAGMDTLIMHLCEETA---PENQKFILQEDGSLFHEQSKKCVQ 1708
KEIR+N+ E C V D + M C + P N + +EDG++FH ++ C+
Sbjct: 491 NKEIRFNS-VTELCAEVPQOKDYVGMQNCPKDGLFVPVNI IWHFKEDGTIFHPHTRLCLS 549

Query: 1709 AARKESDVSFVPLLRDCTNSD-HQKWFFKE 1795

A R V + + C D +Q W F++

Sbjct: 550 AYRTAEGRPVHM-KTCDALDKNQLWRFKE 578

>gi|1934912|emb|CAA69875| (Y08564) UDP-GalNAc:polypeptide
N-acetylgalactosaminyltransferase [Homo sapiens]
Length = 578

Plus Strand HSPs:

Score = 1617 (574.3 bits), Expect = 3.0e-165, P = 3.0e-165
Identities = 322/570 (56%), Positives = 399/570 (70%), Frame = +2

Query: 128 VLLALLALAG-----LGSVLRAQRGAGAGAAEPGPRTTPRGRR-----EPVMRPPVPA 277
+LLA L +A L S A GAG A E G R + P+ +PP +

Sbjct: 13 LLLAFLTVAIFYVELLVSTFHASAGAGR-ARELGSRRLSDLQKNTEDLSRPLYKKPPADS 71

Query: 278 NALGARGEAVRLQLQGEELRLQEESVRLHQINIYLSDRISLHRRLPXRWNPLCKEKKYDY 457
ALG G+A +LQL +EL+ QEE + + INIYLSDRISLHR + + CK +K++Y

Sbjct: 72 RALGEWGKASKLQLNEDELKQQEELIERYAINIYLSDRISLHRHIEDKRMYECKSQKFNY 131

Query: 458 DNLPRTSVIIAFYNEAWSTLLRTVYSVLETS PDILLEEVILVDDYSDREHLKERLANELS 637
LP TSVIIAFYNEAWSTLLRT++SVLETS P +LL+E+ILVDD SDR +LK +L +S

Sbjct: 132 RTLPTTSVIIAFYNEAWSTLLRTIHSVLETS PAVLLKEIILVDDLSDRVYLKTQLETYIS 191

Query: 638 GLPKVRLIRANKREGLVRARLLGASAARGDVLTFDCHCECHGWLEPLLQRIHEEESAV 817
L +VRLIR NKREGLVRARL+GA+ A GDVLTFL CHCE+ GWLEPLL+RI E+AV

Sbjct: 192 NLDVRVRLIRTNKREGLVRARLIGATFATGDVLTFLYCHCECN SGWLEPLLRI GR YETAV 251

Query: 818 VCPVIDVIDWNTFEYLGNSGEPQIGGFDWRVLVFTWHTVPERERIRMQSPVDVIRSPTMAG 997
VCPVID IDWNTFE+ GEP IGGFDWR L F WH+VP++ER R S +D IRSPTMAG

Sbjct: 252 VCPVIDTIDWNTFEFYMQIGPEMIGGFDWR LTFQWHSVPKQERDRRISRIDPIRSPTMAG 311

Query: 998 GLFAVSKKYFEYLGSYDTGMEVWGGENLEFSFRIWQCGGVLETHPCSHVGHVFRKQAPYS 1177
GLFAVSKKYF+YLG+YDTGMEVWGGENLE SFR+WQCGG LE HPCSHVGHVF K+APY+

Sbjct: 312 GLFAVSKKYFQYLGTYDTGMEVWGGENLELSFRVWQCGGKLEIHPCHVGHVFPKRAPYA 371

Query: 1178 RNKALANSVXAAEVWMDEFKELYHNRNPRARLEPFGDVTERKQLRDKLQCKDKFWFLETV 1357
R L N+ AAEVWMDE+KE +Y+RNP AR E +GD++ERK LR++L+CK F W+L+ V

Sbjct: 372 RPNFLQNTARAAEVWMDEYKEHFYNRNPPARKEAYGDISERKLLRERLRCKSFWDYLVKNV 431

Query: 1358 YPELHVPEDRPGFFGMLQNKGLTDYCFDYNPPDENQIVGHQVILYLCHGMGQNQFFEYTS 1537
+P LHPEDRPG+ G ++++G++ C DYN PD N G + L+ CHG G NQFFEYTS

Sbjct: 432 FPNLHVPEDRPGWHGAIRSRGISSECLDYNPDNNP-TGANLSLFGCHGQGGNQFFEYTS 490

Query: 1538 QKEIRYNTHQPEGCIAVEAGMDTLIMHLCEETA---PENQKFILQEDGSLFHEQSKKCVQ 1708

KEIR+N+ E C V + + M C + P N + +EDG++FH S C+
Sbjct: 491 NKEIRFNS-VTELCAEVPEQKNYVGMQNC PKDGFVPANIWHFKEDGTIFHPHSGLCLS 549

Query: 1709 AARKESSDSFVPLLRDCTNSD-HQKWFFKE 1795

A R V + R C D +Q W F++

Sbjct: 550 AYRTPEGRPDVQM-RTCDALDKNQIWSFEK 578

>gi|10437274|dbj|BAB15027| (AK024865) unnamed protein product [Homo sapiens]
Length = 284

Plus Strand HSPs:

Score = 1547 (549.6 bits), Expect = 8.0e-158, P = 8.0e-158
Identities = 282/284 (99%), Positives = 282/284 (99%), Frame = +2

Query: 953 MQSPVDVIRSPTMAGGLFAVSKKYFEYLGSYDTGMEVWGGENLEFSFRIWQCGGVLETHP 1132

MQSPVDVIRSPTMAGGLFAVSKKYFEYLGSYDTGMEVWGGENLEFSFRIWQCGGVLETHP

Sbjct: 1 MQSPVDVIRSPTMAGGLFAVSKKYFEYLGSYDTGMEVWGGENLEFSFRIWQCGGVLETHP 60

Query: 1133 CSHVGHVFRKQAPYSRNKALANSVXAAEVWMDEFKELYHRNPRARLEPFGDVTERKQLR 1312

CSHVGHVF KQAPYSRNKALANSV AAEVWMDEFKELYHRNPRARLEPFGDVTERKQLR

Sbjct: 61 CSHVGHVFPKQAPYSRNKALANSVRAAEVWMDEFKELYHRNPRARLEPFGDVTERKQLR 120

Query: 1313 DKLQCKDFKWFLFETVYPELHVPEDRPGFFGMLQNKGLTDYCFDYNPPDENQIVGHQVILY 1492

DKLQCKDFKWFLFETVYPELHVPEDRPGFFGMLQNKGLTDYCFDYNPPDENQIVGHQVILY

Sbjct: 121 DKLQCKDFKWFLFETVYPELHVPEDRPGFFGMLQNKGLTDYCFDYNPPDENQIVGHQVILY 180

Query: 1493 LCHGMGQNQFFEYTSQKEIRYNTHQPEGCIAVEAGMDTLIMHLCEETAPENQKFILQEDG 1672

LCHGMGQNQFFEYTSQKEIRYNTHQPEGCIAVEAGMDTLIMHLCEETAPENQKFILQEDG

Sbjct: 181 LCHGMGQNQFFEYTSQKEIRYNTHQPEGCIAVEAGMDTLIMHLCEETAPENQKFILQEDG 240

Query: 1673 SLFHEQSKKCVQAARKESSDSFVPLLRDCTNSDHQKWFFKERML 1804

SLFHEQSKKCVQAARKESSDSFVPLLRDCTNSDHQKWFFKERML

Sbjct: 241 SLFHEQSKKCVQAARKESSDSFVPLLRDCTNSDHQKWFFKERML 284

>gi|5834600|emb|CAA69876| (Y08565) UDP-GalNAc:polypeptide
N-acetylgalactosaminyltransferase [Homo sapiens]
Length = 622

Plus Strand HSPs:

Score = 40 (19.1 bits), Expect = 9.9e-120, Sum P(2) = 9.9e-120
Identities = 8/14 (57%), Positives = 9/14 (64%), Frame = +3

Query: 204 PSRDPRAPRAPGGA 245

P +DP AP A G A

Sbjct: 106 PPQDPNAPGADGKA 119

Score = 1168 (416.2 bits), Expect = 9.9e-120, Sum P(2) = 9.9e-120
Identities = 246/537 (45%), Positives = 338/537 (62%), Frame = +2

Query: 233 PGRREPVMPPVPANALGARGEAV-RLQLQGEELRLQEESVRLHQINIYLSDRISLHRR 409
P +P RPP NA GA G+A + + E + +EE + H N + SDRISL R
Sbjct: 96 PAELKPFWERPPQDPNAPGADGKAFQKSKWTPLETQEKEEGYKKHCFNAFASDRISLQRS 155

Query: 410 L-PXRWNPLCKEKKYDY-DNLPRTSVIIAFYNEAWSTLLRTVYSVLETSPDILLEEVILV 583
L P P C ++K+ L TSVII F+NEAWSTLLRTVYSVL T+P ILL+E+ILV
Sbjct: 156 LGPDTRPPECVDQKFRRCPPLATTSVIIIVFHNEAWSTLLRTVYSVLHTTPAILLKEIILV 215

Query: 584 DDYSDREHLKERLANELSGLPKVRLIRANKREGLVRARLLGASAARGDVLTFDCHCECH 763
DD S EHLKE+L + L VR++R +R+GL+ ARLLGAS A+ +VLTFD HCEC
Sbjct: 216 DDASTEHLKEKLEQYVKQLQVVRVVRQEERKGLITARLLGASVAQAEVLTFDHAHCECF 275

Query: 764 EGWLEPLLQRIHEEESAVVCPVIDVIDWNTFEYLGNSGEPQI---GGFDWRLVFTWHTVP 934
GWLEPLL RI E+++ VV P I ID NTFE+ ++ G FDW L F W T+P
Sbjct: 276 HGWLEPLLARIAEDKTVVVSPIVITIDLNTFEFAKPVQGRVHSRGNFDWSLTFGWETLP 335

Query: 935 ERERIRMQSPVDVIRSPTMAGGLFAVSKKYFEYLGSYDTGMEVWGGENLEFSFRIWQCGG 1114
E+ R + I+SPT AGGLF++ K YFE++G+YD ME+WGGEN+E SFR+WQCGG
Sbjct: 336 PHEKQRRKDETYPIKSPTFAGGLFSIPKSYFEHIGTYDNQMEIWGGENVMSFRVWQCGG 395

Query: 1115 VLETHPCSHVGHVFRKQAPYSRNKALA----NSVXAAEVWMDDEFKELYHRNPRA----R 1270
LE PCS VGHVFR ++P++ K + N V AEVWMD +K+++Y RN +A +
Sbjct: 396 QLEIIPCSVVGHVFRKSPHTFPKGTSVIARNQVRLAEVWMDSYKKIFYRRNLQAAKMAQ 455

Query: 1271 LEPFGDVTERKQLRDKLQCKDFKWFLFETVYPELHVPEDRPGFFGMLQNKGLTDYCFDYNP 1450
+ FGD++ER QLR++L C +F W+L VYPE+ VP+ P F+G ++N G T+ C D
Sbjct: 456 EKSFGDISERLQLREQLHCHNFSWYLNHNVPEMFVPDLTPTFYGAIKNLG-TNQCLDVG- 513

Query: 1451 PDENQIVGHQVILYLCHGMGQNPFFEYTSQKEIRYNTHQPEGCIAVEAGMDTL-IMHLCE 1627
EN G +I+Y CHG+G NQ+FEYT+Q+++R+N + + C+ V G L H
Sbjct: 514 --ENNRRGGKPLIMYSCHGLGNGYFEYTTQORDLRHNIAC-QLCLHVSKGALGLGSCHFTG 570

Query: 1628 ETA--PENQKFILQEDGSLFHEQSKKCVQAARKESSDSFVPLLRDCTNSD-HQKWFF 1789
+ + P++++ L +D + + S C+ + K+ P + C SD HQ W F
Sbjct: 571 KNSQVPKDEEWELAQDQLIRNSGSGTCLTSQDKK-----PAMAPCNPSDPHQLWLF 621

>gi|3047191|gb|AAC13671| (AF031835) GLY5a; ppGaNtase [Caenorhabditis elegans]
>pir|T42245|T42245 probable polypeptide
N-acetylgalactosaminyltransferase (EC 2.4.1.41) - Caenorhabditis
elegans
Length = 623

Plus Strand HSPs:

Score = 1185 (422.2 bits), Expect = 1.8e-119, P = 1.8e-119
Identities = 252/530 (47%), Positives = 326/530 (61%), Frame = +2

Query: 251 VMPPFPV----PANALGARGEAV---RLQLQGEELRLQEE SVRLHQINIYLSDRISLHRR 409
V P P+ A G G+AV ++ + + N Y SD IS+HR
Sbjct: 97 VDPNDPIYKKGDAAQAGELGKAVVVDKTKLSTEEKAKYDKGMLNNAFNQYASDMISVHRT 156

Query: 410 LPXRWNPLCKEKKYDYDNLPRTSVIIAFYNEAWSTLLRTVYSVLETSPDILLEEVILVDD 589
LP + CK +KY+ +NLPRTSVII F+NEAWS LLRTV+SVLE +PD LLEEV+LVDD
Sbjct: 157 LPTNIDAECKTEKYN-ENLPRTSVIICFHNEAWSVLLRTVHSLVLETPDHLLEEVVLVDD 215

Query: 590 YSDREHLKERLANELSGLP-KVRLIRANKREGLVRARLLGASAARGDVLTFDCHCECHE 766
+SD +H K L +S KV+++R KREGL+RARL GA+ A G+VLT+LD HCEC E
Sbjct: 216 FSDMDHTKRPLEEYMSQFGGKVKILRMEKREGLIRARLRGA AVATGEVLT YLD SHCECME 275

Query: 767 GWLEPLLQRIHEEESAVVCPVIDVIDWNTFEYLGNSGE-PQIGGFDWRLVFTWHTVPERE 943
GW+EPLL RI + + VVCPVIDVID NTFEY + +GGFDW L F WH++PER+
Sbjct: 276 GWMEPLLDRIKRDPTTVVCPVIDVIDNTFEYHHSKAYFTSVGGFDWGLQFNWHSIPERD 335

Query: 944 RIRMQSPVDVIRSPTMAGGLFAVSKKYFEYLGSYDTGMEVWGGENLEFSFRIWQCGGVLE 1123
R P+D +RSPTMAGGLF++ K+YFE LG+YD G ++WGGENLE SF+IW CGG LE
Sbjct: 336 RKNRTRPIDPVRSPPTMAGGLFSIDKEYFEKLGTYDPGFDIWGGENLELSFKIWMCGGTLE 395

Query: 1124 THPCSHVGHVFRKQAPYS-R---NKALANSVXAAEVWMEDEFKELYHNRNPRARLEPFGDV 1291
PCSHVGHVFRK++PY R N NS+ AEWV+D++K YY R +L FGD+
Sbjct: 396 IVPCSHVGHVFRKRSPYKWRGTGVNVLRNSIRLAEVWLDYKTYYYERINN-QLGDFGDI 454

Query: 1292 TERKQLRDKLQCKDFKWFLETVPYELHVPEDRPGFFGMLQNKGLTDYCFDYNPPDENQIV 1471
+ RK+LR+ L CK FKW+L+ +YPEL VP + M G C DY P
Sbjct: 455 SSRKKLREDLGCKSFKWYLDNIYPELFPGESVAKGEMRNAGGKNRQCIDYKPSG----- 509

Query: 1472 GHQVILYLCHGMGQNQFFEYTSQKEIRYNTHQPEGCIAVEAGMDTLIMHLCEETAPENQK 1651
G V +Y CH G NQ++ + EIR + E C+ AG D ++ C NQ+
Sbjct: 510 GKTVMGYQCHNQGGNQYWMLSKDGEIR----RDESCVDY-AGSDVMVFP-CHGMKG-NQE 562

Query: 1652 FILQED-GSLFHEQSKKCVQAARKESSDSFVPLLRDCTNSD-HQKWFFKE 1795
+ D G L H S+KC+ + + V C D +Q W FKE
Sbjct: 563 WRYNHDTGRLQHAVSQKCLGMTKDGAKLEMVA----CQYDDPYQHWKFKE 608